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#Simulates human for 2 weeks using mouse study protocol (6 hr/day 5
days/week)
#Uses metabolism constants from Table 3 Yang et al.

#Set the working directory to where you downloaded the scripts
setwd(dirname(parent.frame(2)$ofile))

#Load libraries needed to run scenario
library(deSolve)

#Model path and name
mName <- "chloroprene.model"

#Load model inits file for the ode solver
source(paste0(mName, "_inits.R"))

#Load the model dll
dyn.load(paste0(mName, .Platform$dynlib.ext))

#Scenario specific values
tstart <- 0.0
tstop <- 336
times <- seq(tstart, tstop , by=0.01)

#Physiological parameters path

#Load the parameters
source('./params/Human_3.R')
source('./states.R')

#Timing variables for forcing functions
dstart <- tstart
dlength <- 6      #hours per day to expose
ddaysperwk <- 5   #days of week to expose
dexpend <- 12     #days of exposure
parms["TSTOP"] <- tstop

#Source forcing functions
#This loads the function forcing() in the namespace
source("forfunc.R")

#Scenario Specific Exposure
parms["CONC"]<- 12.3

ppm <- c(12.3, 32.0, 80.0)
cinh1 <- data.frame(ppm)
cinh <- lapply(cinh1, as.numeric)
outlist <- list()
ppm2 <- list()

for(i in 1:nrow(cinh1)){

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parms["CONC"] <- cinh1[i,]

{
  out <-ode(Y, times, func = "derivs", parms = parms, method="vode",
atol=1.0e-9, rtol=1.0e-6,
            dllname = mName, initforc="initforc", forcings=forcings,
initfunc = "initmod", nout = length(Outputs),
            fcontrol=list(method="linear"), outnames = Outputs)

}
outlist[[i]] <- out[33601,]
}
frout1 <- data.frame(outlist)
dout <- data.frame(t(frout1), row.names=paste(1:3))
rout <- cbind(dout[,c(21,22,23,24)])  

  

"Human Table 3"
rout
  

  

#load the model dll
dyn.unload(paste0(mName,.Platform$dynlib.ext))
```